# FIG. 1A

```
  1 GGATAAGCCT GGGGCCAGCA TGAGCCAGAG GGAGGGAAGT CTGGAAGACC
    CCTATTCGGA CCCCGGTCGT ACTCGGTCTC CCTCCCTTCA GACCTTCTGG
  1                       M   S  Q  R   E  G  S   L  E  D  H

 51 ACCAGACTGA CTCCTCAATC TCATTCCTAC CCCATTTGGA GGCCAAGATC
    TGGTCTGACT GAGGAGTTAG AGTAAGGATG GGGTAAACCT CCGGTTCTAG
 12   Q  T  D   S  S  I   S  F  L  P   H  L  E   A  K  I

101 CGCCAGACAC ACAACCTTGC CCGCCTCCTG ACCAAATATG CAGAACAACT
    GCGGTCTGTG TGTTGGAACG GGCGGAGGAC TGGTTTATAC GTCTTGTTGA
 28 R  Q  T  H   N  L  A   R  L  L   T  K  Y  A   E  Q  L

151 TCTGGAGGAA TACGTGCAGC AACAGGGAGA GCCCTTTGGG CTGCCGGGCT
    AGACCTCCTT ATGCACGTCG TTGTCCCTCT CGGGAAACCC GACGGCCCGA
 45   L  E  E   Y  V  Q  Q   Q  G  E   P  F  G   L  P  G  F

201 TCTCACCACC GCGGCTGCCG CTGGCCGGCC TGAGTGGCCC GGCTCCGAGC
    AGAGTGGTGG CGCCGACGGC GACCGGCCGG ACTCACCGGG CCGAGGCTCG
 62   S  P  P   R  L  P   L  A  G  L   S  G  P   A  P  S

251 CATGCAGGGC TACCGGTGTC CGAGCGGCTG CGGCAGGATG CAGCCGCCCT
    GTACGTCCCG ATGGCCACAG GCTCGCCGAC GCCGTCCTAC GTCGGCGGGA
 78 H  A  G  L   P  V  S   E  R  L   R  Q  D  A   A  A  L

301 GAGTGTGCTG CCCGCGCTGT TGGATGCCGT CCGCCGCCGC CAGGCGGAGC
    CTCACACGAC GGGCGCGACA ACCTACGGCA GGCGGCGGCG GTCCGCCTCG
 95   S  V  L   P  A  L  L   D  A  V   R  R  R   Q  A  E  L

351 TGAACCCGCG CGCCCCGCGC CTGCTGCGGA GCCTGGAGGA CGCAGCCCGC
    ACTTGGGCGC GCGGGGCGCG GACGACGCCT CGGACCTCCT GCGTCGGGCG
112   N  P  R   A  P  R   L  L  R  S   L  E  D   A  A  R

401 CAGGTTCGGG CCCTGGGCGC CGCGGTGGAG ACAGTGCTGG CCGCGCTGGG
    GTCCAAGCCC GGGACCCGCG GCGCCACCTC TGTCACGACC GGCGCGACCC
128 Q  V  R  A   L  G  A   A  V  E   T  V  L  A   A  L  G

451 CGCTGCAGCC CGCGGGCCCG GGCCAGAGCC CGTCACCGTC GCCACCCTCT
    GCGACGTCGG GCGCCCGGGC CCGGTCTCGG GCAGTGGCAG CGGTGGGAGA
145   A  A  A   R  G  P  G   P  E  P   V  T  V   A  T  L  F

501 TCACGGCCAA CAGCACTGCA GGCATCTTCT CAGCCAAGGT GCTGGGGTTC
    AGTGCCGGTT GTCGTGACGT CCGTAGAAGA GTCGGTTCCA CGACCCCAAG
162   T  A  N   S  T  A   G  I  F  S   A  K  V   L  G  F

551 CACGTGTGCG GCCTCTATGG CGAGTGGGTG AGCCGCACAG AGGGCGACCT
    GTGCACACGC CGGAGATACC GCTCACCCAC TCGGCGTGTC TCCCGCTGGA
178 H  V  C  G   L  Y  G   E  W  V   S  R  T  E   G  D  L

601 GGGCCAGCTG GTGCCAGGGG GCGTCGCCTG AGAGTGAATA CTTTTTCTTG
    CCCGGTCGAC CACGGTCCCC CGCAGCGGAC TCTCACTTAT GAAAAAGAAC
195   G  Q  L   V  P  G  G   V  A  O
```

# FIG. 1B

```
 651 TAAGCTCGCT CTGTCTCGCC TCTTTGGCTT CAAATTTTCT GTCTCTCCAT
     ATTCGAGCGA GACAGAGCGG AGAAACCGAA GTTTAAAAGA CAGAGAGGTA

 701 CTGTGTCCTG TGTGTTCTTG GGCTGTCCCT ATCTTTCTGC ATTTGTGTGG
     GACACAGGAC ACACAAGAAC CCGACAGGGA TAGAAAGACG TAAACACACC

 751 TCTCTCTCTT CTGCTCTCCT CTCTGCAGGG AGCTTCTTTT TTCCAACAGT
     AGAGAGAGAA GACGAGAGGA GAGACGTCCC TCGAAGAAAA AAGGTTGTCA

 801 TTCTCGTTTT GTCTCTCTCC AGTCTTGAAC ACTTTTGTCT CCGAGAGGTC
     AAGAGCAAAA CAGAGAGAGG TCAGAACTTG TGAAAACAGA GGCTCTCCAG

 851 TCTTTTTGTT TCCTTGTCTC TTGGTTCTTT CTTTGCTTGC TTGCTTGCTT
     AGAAAAACAA AGGAACAGAG AACCAAGAAA GAAACGAACG AACGAACGAA

 901 GCTTGCTTGT TGTTGAGACA GGGTCTCACC ATATAGCTCT GGATGGCCTG
     CGAACGAACA ACAACTCTGT CCCAGAGTGG TATATCGAGA CCTACCGGAC

 951 GAACTTGCTA TGTAGGCCAG GCTGGCCTCC AGCTCATAGA GATCCACTTG
     CTTGAACGAT ACATCCGGTC CGACCGGAGG TCGAGTATCT CTAGGTGAAC

1001 CCTCCGACTC CCAATTTCCC CATCTGTCTC CCTGTGATCC ATATGGGTAT
     GGAGGCTGAG GGTTAAAGGG GTAGACAGAG GGACACTAGG TATACCCATA

1051 GTGTAACCCT TACTTTGTCT CATGGAGGTG ACAATTTTTC TCCCTTCAGT
     CACATTGGGA ATGAAACAGA GTACCTCCAC TGTTAAAAAG AGGGAAGTCA

1101 TTCTTTGTTC TTTACTGACC AGAAAAGTGC CTACTTGTCC CCTGGTGGCA
     AAGAAACAAG AAATGACTGG TCTTTTCACG GATGAACAGG GGACCACCGT

1151 AGGCCATTCA CCTTAGGACC TTCCCACCAG TTCCTTTGTA GGCAAATCCC
     TCCGGTAAGT GGAATCCTGG AAGGGTGGTC AAGGAAACAT CCGTTTAGGG

1201 TCCCCCTTTG AGGTCCTTCC CTTTCATACC GCCCTAGGCT GGTCAATGGA
     AGGGGGAAAC TCCAGGAAGG GAAAGTATGG CGGGATCCGA CCAGTTACCT

1251 GAGAGAAAGG CAGAAAAACA TCTTTAAAGA GTTTTATTTG AGAATAAATT
     CTCTCTTTCC GTCTTTTTGT AGAAATTTCT CAAAATAAAC TCTTATTTAA

1301 AATTTTTGTA AATAAAATGT TTAACAATAA AACTAAACTT TTATGAAAAA
     TTAAAAACAT TTATTTTACA AATTGTTATT TTGATTTGAA AATACTTTTT

1351 AA (polyA)
     TT
```

# FIG. 2

```
                10        20        30        40        50
chf.781  MSQREGSLEDHQTDSSISFLPHLEAKIRQTHNLARLLTKYAEQLLEEYVQ
                          **        ***         * * **
humcntf            MAFTEHSPLTPHRRDLCSRSIWLARKIRSDLTALTESYVK
                          10        20        30        40

                60        70        80        90       100
chf.781  QQGEPFGLPGFSPPRLPLAGLSGPAPSHAGLPVSERLRQDAAALSVLPAL
          **        *    * *                ***     *       *
humcntf  HQGLNKNINLDSADGMPVA----STDQWSELTEAERLQENLQAYRTFHVL
                50              60        70        80

                110       120       130       140
chf.781  LD-AVRRRQAELNPRAPRLLRSLEDAARQVRALGAAVETVLAALGAAARG
         *       *    *                ** *     *     *
humcntf  LARLLEDQQVHFTPTEGDFHQAIHTLLLQVAAFAYQIEELMILLEYKIPR
           90       100       110       120       130

       150       160       170       180       190
chf.781  PGPEPVTVATLFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLGQLVP
                          * *  *  *  *       *  *   **
humcntf  NEADGMPINV-----GDGGLFEKKLWGLKVLQELSQWTVRSIHDL-RFIS
          140             150       160       170       180

       200
chf.781  GGVAO

humcntf  SHQTGIPARGSHYIANNKKM
                190       200
```

# FIG. 3

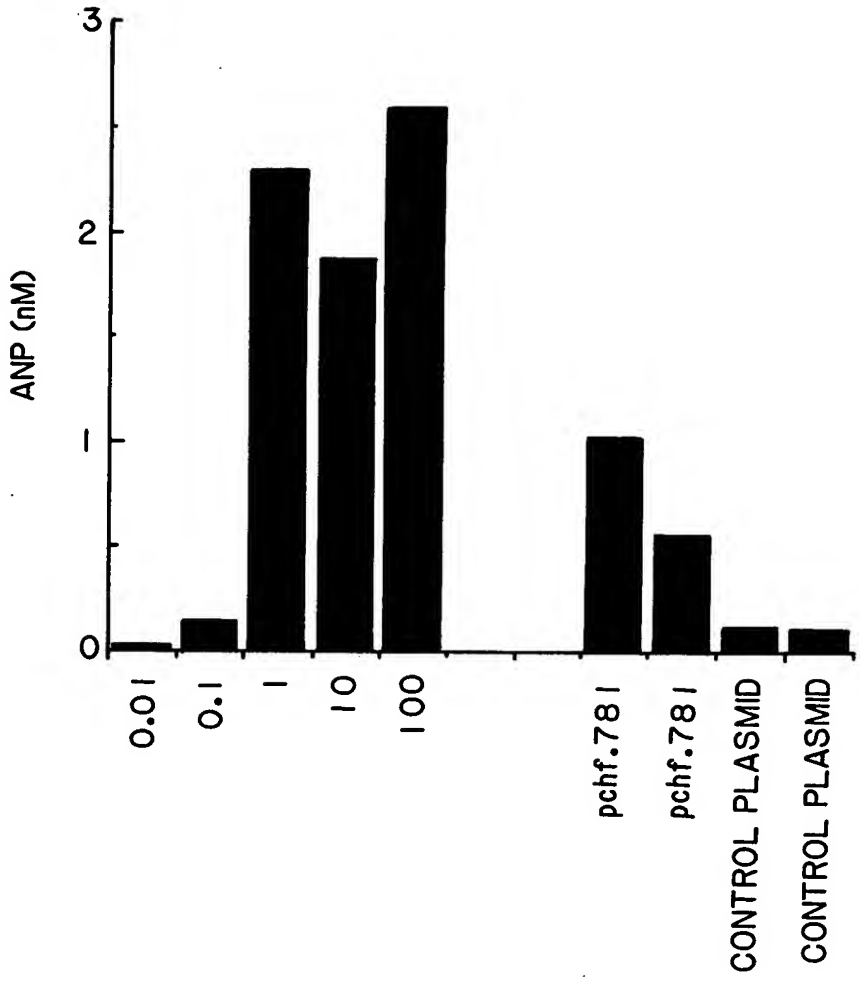
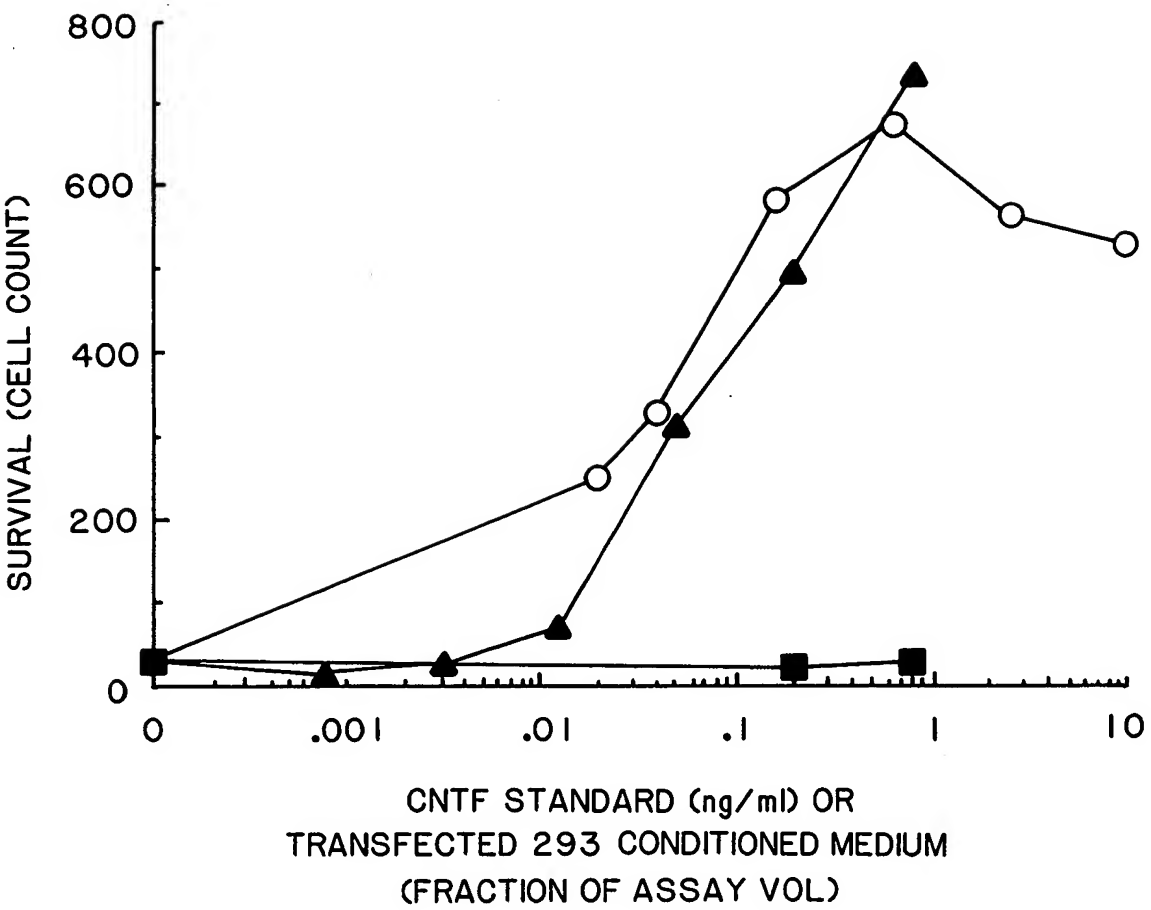

ANP (nM)
3
2
1
0
0.01
0.1
1
10
100
pchf.781
pchf.781
CONTROL PLASMID
CONTROL PLASMID
PHENYLEPHRINE (uM)
STANDARD CURVE
293 TRANSFECTION

FIG. 4


800
600
400
200
0
SURVIVAL (CELL COUNT)
0
.001
.01
.1
1
10
CNTF STANDARD (ng/ml) OR
TRANSFECTED 293 CONDITIONED MEDIUM
(FRACTION OF ASSAY VOL)

# FIG. 5A

```
  1  GTGAAGGGAG CCGGGATCAG CCAGGGGCCA GCATGAGCCG GAGGGAGGGA
     CACTTCCCTC GGCCCTAGTC GGTCCCCGGT CGTACTCGGC CTCCCTCCCT
  1                                     M  S  R   R  E  G

 51  AGTCTGGAAG ACCCCCAGAC TGATTCCTCA GTCTCACTTC TTCCCCACTT
     TCAGACCTTC TGGGGGTCTG ACTAAGGAGT CAGAGTGAAG AAGGGGTGAA
  7  S  L  E  D   P  Q  T   D  S  S   V  S  L  L   P  H  L

101  GGAGGCCAAG ATCCGTCAGA CACACAGCCT TGCGCACCTC CTCACCAAAT
     CCTCCGGTTC TAGGCAGTCT GTGTGTCGGA ACGCGTGGAG GAGTGGTTTA
 24   E  A  K   I  R  Q  T   H  S  L   A  H  L   L  T  K  Y

151  ACGCTGAGCA GCTGCTCCAG GAATATGTGC AGCTCCAGGG AGACCCCTTC
     TGCGACTCGT CGACGAGGTC CTTATACACG TCGAGGTCCC TCTGGGGAAG
 41   A  E  Q   L  L  Q   E  Y  V  Q   L  Q  G   D  P  F

201  GGGCTGCCCA GCTTCTCGCC GCCGCGGCTG CCGGTGGCCG GCCTGAGCGC
     CCCGACGGGT CGAAGAGCGG CGGCGCCGAC GGCCACCGGC CGGACTCGCG
 57  G  L  P  S   F  S  P   P  R  L   P  V  A  G   L  S  A

251  CCCGGCTCCG AGCCACGCGG GGCTGCCAGT GCACGAGCGG CTGCGGCTGG
     GGGCCGAGGC TCGGTGCGCC CCGACGGTCA CGTGCTCGCC GACGCCGACC
 74   P  A  P   S  H  A  G   L  P  V   H  E  R   L  R  L  D

301  ACGCGGCGGC GCTGGCCGCG CTGCCCCCGC TGCTGGACGC AGTGTGTCGC
     TGCGCCGCCG CGACCGGCGC GACGGGGGCG ACGACCTGCG TCACACAGCG
 91   A  A  A   L  A  A   L  P  P  L   L  D  A   V  C  R

351  CGCCAGGCCG AGCTGAACCC GCGCGCGCCG CGCCTGCTGC GCCGCCTGGA
     GCGGTCCGGC TCGACTTGGG CGCGCGCGGC GCGGACGACG CGGCGGACCT
107  R  Q  A  E   L  N  P   R  A  P   R  L  L  R   R  L  E

401  GGACGCGGCG CGCCAGGCCC GGGCCCTGGG CGCCGCCGTG GAGGCCTTGC
     CCTGCGCCGC GCGGTCCGGG CCCGGGACCC GCGGCGGCAC CTCCGGAACG
124   D  A  A   R  Q  A  R   A  L  G   A  A  V   E  A  L  L

451  TGGCCGCGCT GGGCGCCGCC AACCGCGGGC CCCGGGCCGA GCCCCCCGCC
     ACCGGCGCGA CCCGCGGCGG TTGGCGCCCG GGGCCCGGCT CGGGGGGCGG
141   A  A  L   G  A  A   N  R  G  P   R  A  E   P  P  A
```

# FIG. 5B

```
501  GCCACCGCCT CAGCCGCCTC CGCCACCGGG GTCTTCCCCG CCAAGGTGCT
     CGGTGGCGGA GTCGGCGGAG GCGGTGGCCC CAGAAGGGGC GGTTCCACGA
157  A  T  A  S   A  A  S   A  T  G   V  F  P  A   K  V  L

551  GGGGCTCCGC GTTTGCGGCC TCTACCGCGA GTGGCTGAGC CGCACCGAGG
     CCCCGAGGCG CAAACGCCGG AGATGGCGCT CACCGACTCG GCGTGGCTCC
174   G  L  R   V  C  G  L   Y  R  E   W  L  S   R  T  E  G

601  GCGACCTGGG CCAGCTGCTG CCCGGGGGCT CGGCCTGAGC GCCGCGGGGC
     CGCTGGACCC GGTCGACGAC GGGCCCCCGA GCCGGACTCG CGGCGCCCCG
191    D  L  G   Q  L  L   P  G  G  S   A  O

651  AGCTCGCCCC GCCTCCTCCC GCTGGGTTCC GTCTCTCCTT CCGCTTCTTT
     TCGAGCGGGG CGGAGGAGGG CGACCCAAGG CAGAGAGGAA GGCGAAGAAA

701  GTCTTTCTCT GCCGCTGTCG GTGTCTGTCT GTCTGCTCTT AGCTGTCTCC
     CAGAAAGAGA CGGCGACAGC CACAGACAGA CAGACGAGAA TCGACAGAGG

751  ATTGCCTCGG CCTTCTTTGC TTTTTGTGGG GGAGAGGGGA GGGGACGGGC
     TAACGGAGCC GGAAGAAACG AAAAACACCC CCTCTCCCCT CCCCTGCCCG

801  AGGGTCTCTG TCGCCCAGGC TGGGGTGCAG TGGCGCGATC CCAGCACTGC
     TCCCAGAGAC AGCGGGTCCG ACCCCACGTC ACCGCGCTAG GGTCGTGACG

851  AGCCTCAACC TCCTGGGCTC AAGCCATCCT TCCGCCTCAG CTTCCCCAGC
     TCGGAGTTGG AGGACCCGAG TTCGGTAGGA AGGCGGAGTC GAAGGGGTCG

901  AGCTGGGACT ACAGGCACGC GCCACCACAG CCGGCTAATT TTTTATTTAA
     TCGACCCTGA TGTCCGTGCG CGGTGGTGTC GGCCGATTAA AAAATAAATT

951  TTTTTTGTAG AGACGAGGTT TCGCCATGTT GCCCAGGCTG GTCTTGAACT
     AAAAAACATC TCTGCTCCAA AGCGGTACAA CGGGTCCGAC CAGAACTTGA

1001 CCGGGGCTCA AGCGATCC
     GGCCCCGAGT TCGCTAGG
```

# FIG. 6

```
humct1      1  MSRREGSLEDPQTDSSVSLLPHLEAKIRQTHSLAHLLTKYAEQLLQEYVQLQG
               ** ******* ***** * ************ ** ********** **** **
chf.781     1  MSQREGSLEDHQTDSSISFLPHLEAKIRQTHNLARLLTKYAEQLLEEYVQQQG

humct1     54  DPFGLPSFSPPRLPVAGLSAPAPSHAGLPVHERLRLDAAALAALPPLLDAVCR
                ***** ******* **** ********** **** *****  ** ***** *
chf.781    54  EPFGLPGFSPPRLPLAGLSGPAPSHAGLPVSERLRQDAAALSVLPALLDAVRR

humct1    107  RQAELNPRAPRLLRRLEDAARQARALGAAVEALLAALGAANRGPRAEPPAATA
               ************** ******* ********  ******* ***  **
chf.781   107  RQAELNPRAPRLLRSLEDAARQVRALGAAVETVLAALGAAARGPGPEPVTVAT


humct1    160  --SAASATGVFPAKVLGLRVCGLYREWLSRTEGDLGQLLPGGSA
                  * *  * * *****  ***** ** ********** *** *
chf.781   160  LFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLGQLVPGGVA
```